

AMENDMENTS TO THE CLAIMS

Prior to examination please cancel claims 1-35 and add new claims 36-53.

Claims 1-35 (Cancelled)

Claim 36. (New) A method for obtaining high vigor in a plant cell when compared to a control plant cell, comprising introducing a chimeric gene in said plant cell to yield a transgenic cell, wherein said chimeric gene comprises the following operably linked DNA regions:

- a) a plant-expressible promoter;
- b) a DNA region, which when transcribed yields a RNA molecule, said RNA molecule being capable of reducing the expression of endogenous PARP genes; and
- c) a DNA region involved in transcription termination and polyadenylation wherein said RNA molecule comprises
 - i) a sense nucleotide sequence comprising an nucleotide sequence of about 100 consecutive nucleotides from a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No 1, the nucleotide sequence of SEQ ID No 3, the nucleotide sequence of SEQ ID No 5, or the nucleotide sequence of SEQ ID No 10; and
 - ii) an antisense nucleotide sequence comprising a nucleotide sequence of about 100 consecutive nucleotides from the complement of a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No 1, the nucleotide sequence of SEQ ID No 3, the nucleotide sequence of SEQ ID No 5 or the nucleotide sequence of SEQ ID No 10; said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region; andwherein said vigor of said plant can be measured by measuring the capacity of explants of said plant to reduce 2,3,5-triphenyltetrazoliumchloride.

Claim 37. (New) The method of claim 36, wherein said sense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the nucleotide sequence of SEQ ID No 10 and said antisense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the complement of the nucleotide sequence of SEQ ID No 10.

Claim 38. (New) The method of claim 36, wherein said sense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the nucleotide sequence of SEQ ID No 5 and said antisense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the complement of the nucleotide sequence of SEQ ID No 5.

Claim 39. (New) The method of claim 36, wherein said sense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the nucleotide sequence of SEQ ID No 3 and said antisense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the complement of the nucleotide sequence of SEQ ID No 3.

Claim 40. (New) The method of claim 36, wherein said plant expressible promoter is a constitutive promoter.

Claim 41. (New) The method of claim 36, further comprising the step of regenerating a transgenic plant from said transgenic plant cell.

Claim 42. (New) The method of claim 41, further comprising the step of producing more plants comprising said chimeric gene by a conventional breeding scheme.

Claim 43. (New) The method of claim 41, wherein said plant is selected from the group consisting of corn, oil see rape, linseed, wheat, grass, alfalfa, legume, brassica vegetable, tomato, lettuce, cotton, rice, barley, potato, tobacco, sugar beet, sunflower, carnation, rose, chrysanthemum, tulip.

Claim 44. (New) A transgenic plant exhibiting high vigor when compared to a control plant comprising in its cells a chimeric gene, said chimeric gene comprises the following operably linked DNA regions:

- a) a plant-expressible promoter;
 - b) a DNA region, which when transcribed yields a RNA molecule, said RNA molecule being capable of reducing the expression of endogenous PARP genes; and
 - c) a DNA region involved in transcription termination and polyadenylation;
- wherein said RNA molecule comprises

- i) a sense nucleotide sequence comprising a nucleotide sequence of about 100 consecutive nucleotides from a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No 1, the nucleotide sequence of SEQ ID No 3, the nucleotide sequence of SEQ ID No 5 or the nucleotide sequence of SEQ ID No 10; and
 - ii) an antisense nucleotide sequence comprising a nucleotide sequence of about 100 consecutive nucleotides from the complement of a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No 1, the nucleotide sequence of SEQ ID No 3, the nucleotide sequence of SEQ ID No 5, or the nucleotide sequence of SEQ ID No 10; said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region; and
- wherein said vigor of said plant can be measured by measuring the capacity of explants of said plant to reduce 2, 3, 5-triphenyltetrazoliumchloride.
- said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region; and wherein said vigor of said plant can be measured by measuring the capacity of explants of said plant to reduce 2, 3, 5-triphenyltetrazoliumchloride.

Claim 46. (New) The transgenic plant of claim 45, wherein said sense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the nucleotide sequence of SEQ ID No 10 and said antisense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the complement of the nucleotide sequence of SEQ ID No 10.

Claim 47. (New) The transgenic plant of claim 45, wherein said sense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the nucleotide sequence of SEQ ID No 5 and said antisense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the complement of the nucleotide sequence of SEQ ID No 5.

Claim 48. (New) The transgenic plant of claim 45, wherein said sense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the nucleotide sequence of SEQ

ID No 5 and said antisense nucleotide sequence comprises a nucleotide of about 100 nucleotides selected from the complement of the nucleotide sequence of SEQ ID No 5.

Claim 49. (New) The method of claim 47, wherein said plant expressible promoter is a constitutive promoter.

Claim 50. (New) The transgenic plant of claim 47, wherein said plant is selected from the group consisting of corn, oil seed rape, linseed, wheat, grass, alfalfa, legume, brassica vegetable, tomato, lettuce, cotton, rice, barley, potato, tobacco, sugar beet, sunflower, carnation, rose, chrysanthemum, tulip.

Claim 51. (New) A seed of the plant of claim 47, comprising said chimeric gene.

Claim 52. (New) A chimeric gene comprises the following operably linked DNA regions:

- a) a plant-expressible promoter;
 - b) a DNA region, which when transcribed yields a RNA molecule, said RNA molecule being capable of reducing the expression of endogenous PARP genes; and
 - c) a DNA region involved in transcription termination and polyadenylation;
- wherein said RNA molecule comprises
- i) a sense nucleotide sequence comprising a nucleotide sequence of about 100 consecutive nucleotides from a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No 1, the nucleotide sequence of SEQ ID No 3, the nucleotide sequence of SEQ ID No 5 or the nucleotide sequence of SEQ ID No 10; and
 - ii) an antisense nucleotide sequence comprising a nucleotide sequence of about 100 consecutive nucleotides from the complement of a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No 1, the nucleotide sequence of SEQ ID No 3, the nucleotide sequence of SEQ ID No 5, or the nucleotide sequence of SEQ ID No 10; said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region.

Claim 53. (New) The chimeric gene of claim 52, wherein said plant expressible promoter is a constitutive promoter.